

## RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/540,546  
Source: Ifwo  
Date Processed by STIC: 11/27/06

# ***ENTERED***



IFWO

## RAW SEQUENCE LISTING

DATE: 11/27/2006

PATENT APPLICATION: US/10/540,546

TIME: 14:23:18

Input Set : A:\274130.Substitute.Sequence\_Listing.TXT

Output Set: N:\CRF4\11272006\J540546.raw

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3 <110> APPLICANT: Fujisawa Pharmaceutical Co., Ltd.
4     Matsuoka, Hideaki
5     Fujimura, Takao
6     Hayashi, Masako
7     Aramori, Ichiro
9 <120> TITLE OF INVENTION: New methods for selecting an immunosuppressive agent
11 <130> FILE REFERENCE: 274130USOPCT
W--> 12 <140> CURRENT APPLICATION NUMBER: 10/540,546
13 <141> CURRENT FILING DATE: 2005-06-24
15 <150> PRIOR APPLICATION NUMBER: JP2002-378800
16 <151> PRIOR FILING DATE: 2002-12-27
18 <160> NUMBER OF SEQ ID NOS: 86
20 <170> SOFTWARE: PatentIn version 3.1
22 <210> SEQ ID NO: 1
23 <211> LENGTH: 3255
24 <212> TYPE: DNA
25 <213> ORGANISM: Homo sapiens
27 <220> FEATURE:
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29 <222> LOCATION: (1)..(3255)
30 <223> OTHER INFORMATION: human histone deacetylase-4 (HDAC4) gene
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35 1          5          10          15
37 gtg gag ctg ctg aat cct gcc cgc gtg aac cac atg ccc agc acg gtg      96
38 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
39          20          25          30
41 gat gtg gcc acg gcg ctg cct ctg caa gtg gcc ccc tcg gca gtg ccc      144
42 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
43          35          40          45
45 atg gac ctg cgc ctg gac cac cag ttc tca ctg cct gtg gca gag ccg      192
46 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
47          50          55          60
49 gcc ctg cgg gag cag cag ctg cag cag gag ctc ctg gcg ctc aag cag      240
50 Ala Leu Arg Glu Gln Gln Leu Gln Gln Glu Leu Leu Ala Leu Lys Gln
51 65          70          75          80
53 aag cag cag atc cag agg cag atc ctc atc gct gag ttc cag agg cag      288
54 Lys Gln Gln Ile Gln Arg Gln Ile Leu Ile Ala Glu Phe Gln Arg Gln
55          85          90          95
57 cac gag cag ctc tcc cgg cag cac gag gcg cag ctc cac gag cac atc      336
58 His Glu Gln Leu Ser Arg Gln His Glu Ala Gln Leu His Glu His Ile
59          100          105          110

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61	aag	caa	caa	cag	gag	atg	ctg	gcc	atg	aag	cac	cag	cag	gag	ctg	ctg	384
62	Lys	Gln	Gln	Gln	Glu	Met	Leu	Ala	Met	Lys	His	Gln	Gln	Glu	Leu	Leu	
63		115						120					125				
65	gaa	cac	cag	cgg	aag	ctg	gag	agg	cac	cgc	cag	gag	cag	gag	ctg	gag	432
66	Glu	His	Gln	Arg	Lys	Leu	Glu	Arg	His	Arg	Gln	Glu	Gln	Glu	Leu	Glu	
67		130						135					140				
69	aag	cag	cac	cga	gag	cag	aag	ctg	cag	cag	ctc	aag	aac	aag	gag	aag	480
70	Lys	Gln	His	Arg	Glu	Gln	Lys	Leu	Gln	Gln	Leu	Lys	Asn	Lys	Glu	Lys	
71	145					150					155				160		
73	ggc	aaa	gag	agt	gcc	gtg	gcc	agc	aca	gaa	gtg	aag	atg	aag	tta	caa	528
74	Gly	Lys	Glu	Ser	Ala	Val	Ala	Ser	Thr	Glu	Val	Lys	Met	Lys	Leu	Gln	
75					165						170				175		
77	gaa	ttt	gtc	ctc	aat	aaa	aag	aag	gcg	ctg	gcc	cac	cgg	aat	ctg	aac	576
78	Glu	Phe	Val	Leu	Asn	Lys	Lys	Lys	Ala	Leu	Ala	His	Arg	Asn	Leu	Asn	
79					180						185				190		
81	cac	tgc	att	tcc	agc	gac	cct	cgc	tac	tgg	tac	ggg	aaa	acg	cag	cac	624
82	His	Cys	Ile	Ser	Ser	Asp	Pro	Arg	Tyr	Trp	Tyr	Gly	Lys	Thr	Gln	His	
83		195					200					205					
85	agt	tcc	ctt	gac	cag	agt	tct	cca	ccc	cag	agc	gga	gtg	tcg	acc	tcc	572
86	Ser	Ser	Leu	Asp	Gln	Ser	Ser	Pro	Pro	Gln	Ser	Gly	Val	Ser	Thr	Ser	
87		210					215					220					
89	tat	aac	cac	ccg	gtc	ctg	gga	atg	tac	gac	gcc	aaa	gat	gac	ttc	cct	720
90	Tyr	Asn	His	Pro	Val	Leu	Gly	Met	Tyr	Asp	Ala	Lys	Asp	Asp	Phe	Pro	
91	225					230					235				240		
93	ctt	agg	aaa	aca	gct	tct	gaa	ccg	aat	ctg	aaa	tta	cgg	tcc	agg	cta	768
94	Leu	Arg	Lys	Thr	Ala	Ser	Glu	Pro	Asn	Leu	Lys	Leu	Arg	Ser	Arg	Leu	
95					245						250				255		
97	aag	cag	aaa	gtg	gcc	gaa	aga	cgg	agc	agc	ccc	ctg	tta	cgc	agg	aaa	816
98	Lys	Gln	Lys	Val	Ala	Glu	Arg	Arg	Ser	Ser	Pro	Leu	Leu	Arg	Arg	Lys	
99					260						265				270		
101	gac	ggg	cca	gtg	gtc	act	gct	cta	aaa	aag	cgt	ccg	ttg	gat	gtc	aca	864
102	Asp	Gly	Pro	Val	Val	Thr	Ala	Leu	Lys	Lys	Arg	Pro	Leu	Asp	Val	Thr	
103		275					280					285					
105	gac	tcc	gcg	tgc	agc	agc	gcc	cca	ggc	tcc	gga	ccc	agc	tca	ccc	aac	912
106	Asp	Ser	Ala	Cys	Ser	Ser	Ala	Pro	Gly	Ser	Gly	Pro	Ser	Ser	Pro	Asn	
107		290					295					300					
109	aac	agc	tcc	ggg	agc	gtc	agc	gcg	gag	aac	ggt	atc	gcg	ccc	gcc	gtc	960
110	Asn	Ser	Ser	Gly	Ser	Val	Ser	Ala	Glu	Asn	Gly	Ile	Ala	Pro	Ala	Val	
111	305					310					315				320		
113	ccc	agc	atc	ccg	gcg	gag	acg	agt	ttg	gcg	cac	aga	ctt	gtg	gca	cga	1008
114	Pro	Ser	Ile	Pro	Ala	Glu	Thr	Ser	Leu	Ala	His	Arg	Leu	Val	Ala	Arg	
115					325						330				335		
117	gaa	ggc	tcg	gcc	gct	cca	ctt	ccc	ctc	tac	aca	tcg	cca	tcc	ttg	ccc	1056
118	Glu	Gly	Ser	Ala	Ala	Pro	Leu	Pro	Leu	Tyr	Thr	Ser	Pro	Ser	Leu	Pro	
119					340						345				350		
121	aac	atc	acg	ctg	ggc	ctg	cct	gcc	acc	ggc	ccc	tct	gcg	ggc	acg	gcg	1104
122	Asn	Ile	Thr	Leu	Gly	Leu	Pro	Ala	Thr	Gly	Pro	Ser	Ala	Gly	Thr	Ala	
123					355						360				365		
125	ggc	cag	cag	gac	acc	gag	aga	ctc	acc	ctt	ccc	gcc	ctc	cag	cag	agg	1152

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126	Gly	Gln	Gln	Asp	Thr	Glu	Arg	Leu	Thr	Leu	Pro	Ala	Leu	Gln	Gln	Arg	
127		370					375					380					
129	ctc	tcc	ctt	ttc	ccc	ggc	acc	cac	ctc	act	ccc	tac	ctg	agc	acc	tgc	1200
130	Leu	Ser	Leu	Phe	Pro	Gly	Thr	His	Leu	Thr	Pro	Tyr	Leu	Ser	Thr	Ser	
131	385					390					395				400		
133	ccc	ttg	gag	cgg	gac	gga	ggg	gca	gcg	cac	agc	cct	ctt	ctg	cag	cac	1248
134	Pro	Leu	Glu	Arg	Asp	Gly	Gly	Ala	Ala	His	Ser	Pro	Leu	Leu	Gln	His	
135				405						410					415		
137	atg	gtc	tta	ctg	gag	cag	cca	ccg	gca	caa	gca	ccc	ctc	gtc	aca	ggc	1296
138	Met	Val	Leu	Leu	Glu	Gln	Pro	Pro	Ala	Gln	Ala	Pro	Leu	Val	Thr	Gly	
139				420						425					430		
141	ctg	gga	gca	ctg	ccc	ctc	cac	gca	cag	tcc	ttg	gtt	ggt	gca	gac	cgg	1344
142	Leu	Gly	Ala	Leu	Pro	Leu	His	Ala	Gln	Ser	Leu	Val	Gly	Ala	Asp	Arg	
143			435							440					445		
145	gtg	tcc	ccc	tcc	atc	cac	aag	ctg	cgg	cag	cac	cgc	cca	ctg	ggg	cgg	1392
146	Val	Ser	Pro	Ser	Ile	His	Lys	Leu	Arg	Gln	His	Arg	Pro	Leu	Gly	Arg	
147		450								455					460		
149	acc	cag	tgc	gcc	ccg	ctg	ccc	cag	aac	gcc	cag	gct	ctg	cag	cac	ctg	1440
150	Thr	Gln	Ser	Ala	Pro	Leu	Pro	Gln	Asn	Ala	Gln	Ala	Leu	Gln	His	Leu	
151	465					470					475				480		
153	gtc	atc	cag	cag	cag	cat	cag	cag	ttt	ctg	gag	aaa	cac	aag	cag	cag	1488
154	Val	Ile	Gln	Gln	Gln	His	Gln	Gln	Phe	Leu	Glu	Lys	His	Lys	Gln	Gln	
155				485						490					495		
157	ttc	cag	cag	cag	caa	ctg	cag	atg	aac	aag	atc	atc	ccc	aag	cca	agc	1536
158	Phe	Gln	Gln	Gln	Gln	Leu	Gln	Met	Asn	Lys	Ile	Ile	Pro	Lys	Pro	Ser	
159				500						505					510		
161	gag	cca	gcc	cgg	cag	ccg	gag	agc	cac	ccg	gag	gag	acg	gag	gag	gag	1584
162	Glu	Pro	Ala	Arg	Gln	Pro	Glu	Ser	His	Pro	Glu	Glu	Thr	Glu	Glu	Glu	
163			515							520					525		
165	ctc	cgt	gag	cac	cag	gct	ctg	ctg	gac	gag	ccc	tac	ctg	gac	cgg	ctg	1632
166	Leu	Arg	Glu	His	Gln	Ala	Leu	Leu	Asp	Glu	Pro	Tyr	Leu	Asp	Arg	Leu	
167		530								535					540		
169	ccg	ggg	cag	aag	gag	gcg	cac	gca	cag	gcc	ggc	gtg	cag	gtg	aag	cag	1680
170	Pro	Gly	Gln	Lys	Glu	Ala	His	Ala	Gln	Ala	Gly	Val	Gln	Val	Lys	Gln	
171	545					550					555				560		
173	gag	ccc	att	gag	agc	gat	gag	gaa	gag	gca	gag	ccc	cca	cgg	gag	gtg	1728
174	Glu	Pro	Ile	Glu	Ser	Asp	Glu	Glu	Glu	Ala	Glu	Pro	Pro	Arg	Glu	Val	
175				565						570					575		
177	gag	ccg	ggc	cag	cgc	cag	ccc	agt	gag	cag	gag	ctg	ctc	ttc	aga	cag	1776
178	Glu	Pro	Gly	Gln	Arg	Gln	Pro	Ser	Glu	Gln	Glu	Leu	Leu	Phe	Arg	Gln	
179				580						585					590		
181	caa	gcc	ctc	ctg	ctg	gag	cag	cag	cgg	atc	cac	cag	ctg	agg	aac	tac	1824
182	Gln	Ala	Leu	Leu	Leu	Glu	Gln	Gln	Arg	Ile	His	Gln	Leu	Arg	Asn	Tyr	
183			595							600					605		
185	cag	gcg	tcc	atg	gag	gcc	gcc	ggc	atc	ccc	gtg	tcc	ttc	ggc	ggc	cac	1872
186	Gln	Ala	Ser	Met	Glu	Ala	Ala	Gly	Ile	Pro	Val	Ser	Phe	Gly	Gly	His	
187		610								615					620		
189	agg	cct	ctg	tcc	cgg	gcg	cag	tcc	tca	ccc	gcg	tct	gcc	acc	ttc	ccc	1920
190	Arg	Pro	Leu	Ser	Arg	Ala	Gln	Ser	Ser	Pro	Ala	Ser	Ala	Thr	Phe	Pro	

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191 625          630          635          640
193 gtg tct gtg cag gag ccc ccc acc aag ccg agg ttc acg aca ggc ctc      1968
194 Val Ser Val Gln Glu Pro Pro Thr Lys Pro Arg Phe Thr Thr Gly Leu
195          645          650          655
197 gtg tat gac acg ctg atg ctg aag cac cag tgc acc tgc ggg agt agc      2016
198 Val Tyr Asp Thr Leu Met Leu Lys His Gln Cys Thr Cys Gly Ser Ser
199          660          665          670
201 agc agc cac ccc gag cac gcc ggg agg atc cag agc atc tgg tcc cgc      2064
202 Ser Ser His Pro Glu His Ala Gly Arg Ile Gln Ser Ile Trp Ser Arg
203          675          680          685
205 ctg cag gag acg ggc ctc cgg ggc aaa tgc gag tgc atc cgc gga cgc      2112
206 Leu Gln Glu Thr Gly Leu Arg Gly Lys Cys Glu Cys Ile Arg Gly Arg
207          690          695          700
209 aag gcc acc ctg gag gag cta cag acg gtg cac tcg gaa gcc cac acc      2160
210 Lys Ala Thr Leu Glu Glu Leu Gln Thr Val His Ser Glu Ala His Thr
211 705          710          715          720
213 ctc ctg tat ggc acg aac ccc ctc aac cgg cag aaa ctg gac agt aag      2208
214 Leu Leu Tyr Gly Thr Asn Pro Leu Asn Arg Gln Lys Leu Asp Ser Lys
215          725          730          735
217 aaa ctt cta ggc tcg ctc gcc tcc gtg ttc gtc cgg ctc cct tgc ggt      2256
218 Lys Leu Leu Gly Ser Leu Ala Ser Val Phe Val Arg Leu Pro Cys Gly
219          740          745          750
221 ggt gtt ggg gtg gac agt gac acc ata tgg aac gag gtg cac tcg gcg      2304
222 Gly Val Gly Val Asp Ser Asp Thr Ile Trp Asn Glu Val His Ser Ala
223          755          760          765
225 ggg gca gcc cgc ctg gct gtg ggc tgc gtg gta gag ctg gtc ttc aag      2352
226 Gly Ala Ala Arg Leu Ala Val Gly Cys Val Val Glu Leu Val Phe Lys
227          770          775          780
229 gtg gcc aca ggg gag ctg aag aat ggc ttt gct gtg gtc cgc ccc cct      2400
230 Val Ala Thr Gly Glu Leu Lys Asn Gly Phe Ala Val Val Arg Pro Pro
231 785          790          795          800
233 gga cac cat gcg gag gag agc acg ccc atg ggc ttt tgc tac ttc aac      2448
234 Gly His His Ala Glu Glu Ser Thr Pro Met Gly Phe Cys Tyr Phe Asn
235          805          810          815
237 tcc gtg gcc gtg gca gcc aag ctt ctg cag cag agg ttg agc gtg agc      2496
238 Ser Val Ala Val Ala Ala Lys Leu Leu Gln Gln Arg Leu Ser Val Ser
239          820          825          830
241 aag atc ctc atc gtg gac tgg gac gtg cac cat gga aac ggg acc cag      2544
242 Lys Ile Leu Ile Val Asp Trp Asp Val His His Gly Asn Gly Thr Gln
243          835          840          845
245 cag gct ttc tac agc gac cct agc gtc ctg tac atg tcc ctc cac cgc      2592
246 Gln Ala Phe Tyr Ser Asp Pro Ser Val Leu Tyr Met Ser Leu His Arg
247          850          855          860
249 tac gac gat ggg aac ttc ttc cca ggc agc ggg gct cct gat gag gtg      2640
250 Tyr Asp Asp Gly Asn Phe Phe Pro Gly Ser Gly Ala Pro Asp Glu Val
251 865          870          875          880
253 ggc aca ggg ccc ggc gtg ggt ttc aac gtc aac atg gct ttc acc ggc      2688
254 Gly Thr Gly Pro Gly Val Gly Phe Asn Val Asn Met Ala Phe Thr Gly
255          885          890          895

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257 ggc ctg gac ccc ccc atg gga gac gct gag tac ttg gcg gcc ttc aga      2736
258 Gly Leu Asp Pro Pro Met Gly Asp Ala Glu Tyr Leu Ala Ala Phe Arg
259          900          905          910
261 acg gtg gtc atg ccg atc gcc agc gag ttt gcc ccg gat gtg gtg ctg      2784
262 Thr Val Val Met Pro Ile Ala Ser Glu Phe Ala Pro Asp Val Val Leu
263          915          920          925
265 gtg tca tca ggc ttc gat gcc gtg gag ggc cac ccg acc cct ctt ggg      2832
266 Val Ser Ser Gly Phe Asp Ala Val Glu Gly His Pro Thr Pro Leu Gly
267          930          935          940
269 ggc tac aac ctc tcc gcc aga tgc ttc ggg tac ctg acg aag cag ctg      2880
270 Gly Tyr Asn Leu Ser Ala Arg Cys Phe Gly Tyr Leu Thr Lys Gln Leu
271 945          950          955          960
273 atg ggc ctg gct ggc ggc cgg att gtc ctg gcc ctc gag gga ggc cac      2928
274 Met Gly Leu Ala Gly Gly Arg Ile Val Leu Ala Leu Glu Gly Gly His
275          965          970          975
277 gac ctg acc gcc att tgc gac gcc tcg gaa gca tgt gtt tct gcc ttg      2976
278 Asp Leu Thr Ala Ile Cys Asp Ala Ser Glu Ala Cys Val Ser Ala Leu
279          980          985          990
281 ctg gga aac gag ctt gat cct ctc cca gaa aag gtt tta cag caa aga      3024
282 Leu Gly Asn Glu Leu Asp Pro Leu Pro Glu Lys Val Leu Gln Gln Arg
283          995          1000          1005
285 ccc aat gca aac gct gtc cgt tcc atg gag aaa gtc atg gag atc cac      3072
286 Pro Asn Ala Asn Ala Val Arg Ser Met Glu Lys Val Met Glu Ile His
287          1010          1015          1020
289 agc aag tac tgg cgc tgc ctg cag cgc aca acc tcc aca gcg ggg cgt      3120
290 Ser Lys Tyr Trp Arg Cys Leu Gln Arg Thr Thr Ser Thr Ala Gly Arg
291 1025          1030          1035          1040
293 tct ctg atc gag gct cag act tgc gag aac gaa gaa gcc gag acg gtc      3168
294 Ser Leu Ile Glu Ala Gln Thr Cys Glu Asn Glu Glu Ala Glu Thr Val
295          1045          1050          1055
297 acc gcc atg gcc tcg ctg tcc gtg ggc gtg aag ccc gcc gaa aag aga      3216
298 Thr Ala Met Ala Ser Leu Ser Val Gly Val Lys Pro Ala Glu Lys Arg
299          1060          1065          1070
301 cca gat gag gag ccc atg gaa gag gag ccg ccc ctg tag      3255
302 Pro Asp Glu Glu Pro Met Glu Glu Glu Pro Pro Leu
303          1075          1080
306 <210> SEQ ID NO: 2
307 <211> LENGTH: 1084
308 <212> TYPE: PRT
309 <213> ORGANISM: Homo sapiens
311 <400> SEQUENCE: 2
312 Met Ser Ser Gln Ser His Pro Asp Gly Leu Ser Gly Arg Asp Gln Pro
313 1          5          10          15
315 Val Glu Leu Leu Asn Pro Ala Arg Val Asn His Met Pro Ser Thr Val
316          20          25          30
318 Asp Val Ala Thr Ala Leu Pro Leu Gln Val Ala Pro Ser Ala Val Pro
319          35          40          45
321 Met Asp Leu Arg Leu Asp His Gln Phe Ser Leu Pro Val Ala Glu Pro
322          50          55          60

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RAW SEQUENCE LISTING ERROR SUMMARY  
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:24; N Pos. 4,5,6,7,8,9,12,56

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:60; Line(s) 4155  
Seq#:61; Line(s) 4168  
Seq#:62; Line(s) 4181  
Seq#:63; Line(s) 4194  
Seq#:66; Line(s) 4233  
Seq#:67; Line(s) 4246  
Seq#:68; Line(s) 4259  
Seq#:69; Line(s) 4272  
Seq#:74; Line(s) 4337  
Seq#:75; Line(s) 4350  
Seq#:76; Line(s) 4363  
Seq#:77; Line(s) 4376

**VERIFICATION SUMMARY**

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L:12 M:283 W: Missing Blank Line separator, <140> field identifier

L:3600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0